RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ *10/542,769 A* _____
Source: _____ *PCT* _____
Date Processed by STIC: _____ *03/20/2006* _____

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PCT

RAW SEQUENCE LISTING   DATE: 03/20/2006
PATENT APPLICATION: US/10/542,769A   TIME: 12:14:06

Input Set : A:\WEICK046.APP
Output Set: N:\CRF4\03202006\J542769A.raw

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 3 <110> APPLICANT: BUTZKE, DANIEL
 4        GOEDERT, SIGRID
 5        DITTRICH, MICHAEL
 6        RUDEL, THOMAS
 7        MEYER, THOMAS
 9 <120> TITLE OF INVENTION: L-AMINO ACID OXIDASE WITH CYTOTOXIC ACTIVITY FROM
10        APLYSIA PUNCTATA
12 <130> FILE REFERENCE: WEICKM-0046
14 <140> CURRENT APPLICATION NUMBER: 10/542,769A
15 <141> CURRENT FILING DATE: 2005 07-20
17 <150> PRIOR APPLICATION NUMBER: PCT/EP04/00423
18 <151> PRIOR FILING DATE: 2004-01-20
20 <150> PRIOR APPLICATION NUMBER: EP 03001232.2
21 <151> PRIOR FILING DATE: 2003-01-20
23 <150> PRIOR APPLICATION NUMBER: EP 03026613.4
24 <151> PRIOR FILING DATE: 2003-11-19
26 <160> NUMBER OF SEQ ID NOS: 78
28 <170> SOFTWARE: PatentIn Ver. 3.3
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33 <213> ORGANISM: Aplysia punctata
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45 His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
46          20                  25                  30
48 tgc ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga  144
49 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
50          35                  40                  45
52 gct aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg  192
53 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
54          50                  55                  60
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57 Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
58  65                  70                  75                  80
60 ccc aac aca ccc gac gtt aac ctg gag att ggc ggc atg agg ttc atc  288
61 Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
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(pg-6)

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68 acc ccc aag gtg ttc aag gaa ggt ttc ggc aag gag ggc aga caa aga    384
69 Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
70                     115                  120                  125
72 ttt tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg    432
73 Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
74         130                  135                  140
76 gac gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat    480
77 Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
78 145                  150                  155                  160
80 ctg gtc gaa tac tac ctg gag aaa ctg aca ggt cta caa ctc aac ggc    528
81 Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
82                     165                  170                  175
84 gag ccg ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc    576
85 Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
86                     180                  185                  190
88 aga ttc ctc tat gac ctc tcg ttt gac gaa gcc atg gat ctg gtt gcc    624
89 Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
90         195                  200                  205
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93 Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
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96 gag gtc acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg    720
97 Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
98 225                  230                  235                  240
100 gga gag gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg   768
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102                    245                  250                  255
104 tct tcc gtc cca caa ggg ctc cta cag gct ttt ctg gac gcc gca gac   816
105 Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
106                    260                  265                  270
108 tcc aac gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag   864
109 Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
110         275                  280                  285
112 acc aac ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat   912
113 Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
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120 caa aga gtc atc ctg gcc atg ccg gta tac gct ctg aac caa cta gac  1008
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124 tgg aat cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtt  1056
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132 tgg ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt   1152
133 Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu
134         370                 375                 380
136 ttc agc caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac   1200
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138 385                 390                 395                 400
140 atc ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg   1248
141 Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
142                 405                 410                 415
144 gag ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac   1296
145 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
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149 Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
150         435                 440                 445
152 gag gct tat ggc gtg gag cga gac tcg atc ccg gaa ccc gtg acc gcc   1392
153 Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
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156 gct tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc   1440
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161 Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
162                 485                 490                 495
164 ccg tca ctg aaa gat gag gta tac gtg gtg gga gcc gac tac tcc tgg   1536
165 Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
166         500                 505                 510
168 gga ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac   1584
169 Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn
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192 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
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202             100                 105                 110
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205             115                 120                 125
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214             165                 170                 175
216 Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
217             180                 185                 190
219 Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
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222 Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
223     210                 215                 220
225 Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
226 225                 230                 235                 240
228 Gly Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu
229             245                 250                 255
231 Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
232             260                 265                 270
234 Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
235     275                 280                 285
237 Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
238     290                 295                 300
240 Gly Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala
241 305                 310                 315                 320
243 Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp
244             325                 330                 335
246 Trp Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val
247     340                 345                 350
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250     355                 360                 365
252 Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu
253     370                 375                 380
255 Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr
256 385                 390                 395                 400
258 Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
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261 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
262         420                 425                 430
264 Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
265         435                 440                 445
267 Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
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268      450                     455                     460
270 Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr
271 465                     470                     475                     480
273 Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
274                     485                     490                     495
276 Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
277              500                     505                     510
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301 gcc gac ggt gtc tgc aga aac aga cgt caa tgt aac aga gag gtg tgc     96
302 Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys
303             20                     25                         30
305 ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga gct    144
306 Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
307             35                     40                         45
309 aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc    192
310 Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
311         50                     55                         60
313 gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc    240
314 Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
315 65                     70                     75                     80
317 aac aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag    288
318 Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
319                     85                     90                         95
321 ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc    336
322 Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
323             100                     105                     110
325 ccc aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt    384
326 Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
327         115                     120                     125
329 tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac    432
330 Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
331         130                     135                     140
333 gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg    480
334 Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
335 145                     150                     155                     160
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/20/2006
PATENT APPLICATION: US/10/542,769A   TIME: 12:14:07

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Output Set: **N:\CRF4\03202006\J542769A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:35; Xaa Pos. 5
Seq#:36; Xaa Pos. 6,7
Seq#:42; N Pos. 20,22,58,73,132,150,182,220,254,317,338
Seq#:43; Xaa Pos. 7,8,20,25,44,50,58,59,61,74,85,106,107,112,113,132,133
Seq#:43; Xaa Pos. 137,145
Seq#:44; Xaa Pos. 7,19,24,44,50,61,73,85,106,109,113,127,138
Seq#:45; Xaa Pos. 6,7,19,24,33,44,50,60,73,84,105,112,113,133
Seq#:46; Xaa Pos. 3
Seq#:49; Xaa Pos. 3
Seq#:51; Xaa Pos. 5
Seq#:59; N Pos. 17
Seq#:63; N Pos. 24,25,29,30,34,35
Seq#:76; Xaa Pos. 7,8
Seq#:77; Xaa Pos. 1
Seq#:78; Xaa Pos. 21,22,52,60,69,77

VERIFICATION SUMMARY   DATE: 03/20/2006
PATENT APPLICATION: **US/10/542,769A**   TIME: 12:14:07

Input Set : **A:\WEICK046.APP**
Output Set: **N:\CRF4\03202006\J542769A.raw**

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